TGFb+MMP+ifn b Sequence

10 20 30 40		60	
1234567890 1234567890 1234567890 1234567890			
ATRICOCCOCT COGCCCTCCC CCTCCTCCCCC			60
MetProProS erGlyLeuAr gleuleuPro Leuleuleu	ProLeuLeuTr	pLeuLeuVal	
CIGADGOCIG GOOGGOGGC OGOGGACIA TOCACCIGO			120
LeuThrProG lyProProAl aAlaGlyLeu SerThrCys	LysThrIleAs	pMetGluLeu	
		•	
GIGAAGOGGA AGOGCATOGA GGCCATOCGC GGCCAGATO			180
VallysArgL ysArgIleGl uAlaIleArg GlyGlnIle	L euSerLysLe	uArgLeuAla	
AGCCCCCCGA GCCAGGGGA GGTGCCCCCC GGCCCGCTG			240
SerProProS erGlnGlyGl uValProPro GlyProLeu	P roGluAlaVa	l LeuAlaLeu	
TACAACAGCA COOSCEACOG GGTGGCCGGG GAGAGTGCA			300
TyrAsnSerT hrArgAspAr gValAlaGly GluSerAla	G luProGluPr	· oGluProGlu	
GCCGACTACT ACGCCAAGGA GGTCACCCGC GTGCTAATG			360
AlaAspTyrT yrAlaLysGl uValThrArg ValLeuMet	V alGluThrHi	sAsnGluIle	
TATGACAAGT TCAAGCAGAG TACACAGAC ATATATATC			420
TyrAspLysP heLysGlnSe rThrHisSer IleTyrMet	:P hePheAsnTf	ı rSerGluLeu	
CGAGAACCG TACCIGAACC CGIGITGCIC TCCCGGCA			480
ArgGluAlaV alProGluPr oValLeuLeu SerArgAla	G luLeuArgLe	e uLeuArgArg	
CICAAGITAA AAGIGGAGCA GCACGIGGAG CIGTACCAC			540
Leulysleul ysValGluGl nHisValGlu LeuTyrGl	ıl ystyrsera:	s nAsnSerlip	
COMMACCINAL CONTROL CONTROL CONTROL TO CONTROL			COO
CGATACCICA GCAACCGGCI GCIGGCACCC AGCGACIC			600
ArgTyrLeuS erAsnArgLe uLeuAlaPro SerAspSe	ch Loginizhr	e usermeasp	
OTTONOCCONO INTOTTOCCON ACCOUNTANCE CONTOCNOS	~~ *******	a a	CC0
GICACOGAG TIGIGOGCA GIGGITGAGC CGIGGAGG			660
ValThrGlyV alValArgG1 nTrpLeuSer ArgGlyG1	Ag initeging	i ymeargieu	
ACCOMMENT COMMENTS OF CONCERN A ACCOMMENT	~~ ********	m 03300000000	770
ASCCCCACT CCTCCTGTGA CAGCAGGGAT AACACACT			720
SerAlaHisC ysSerCysAs pSerArgAsp AsmThrLe	ng invaraspr	i eashglypne	
ACTACCOGCC GCCCACCTICA CCTGCCCACC ATTICATOG	03 m03300000	v. mmvvmvvmm	780
ThrThrGlyA rgArgGlyAs pLeuAlaThr IleHisGl			780
minimorya igargoryas predatanic rientsor	ym echsiaigi	ri Orneleuleu	
CICATGGCCA COCCGCTGGA GAGGGCCCAG CATCTGCA	ייינעטעעיינעט עע	(mmonth a	840
LeuMetAlaT hrProLeuGl uArgAlaGln HisLeuGl	ns exclusive	al Acidonalia	040
	in crainties	r Agragraga	
TCCCCCTCS GCCTTTGGGC GGCAGGGGC TCAGCGC	איז שמיזיאליי	יינייבטעיבטעעיי	900
SerProLeuG lyLeuTrpAl aGlyGlyGly SerAlaAl	al latteless	N YEARS INTER	500
Placeriter corlected Setular	ws mirewill	ra resiscamen	
CAGCTOCAAG AAAGGACGAA CATTOGGAAA TGTCAGG	ACC TOCHES	CA OCTGAATGGA	960
GlnLeuGlnG luArgIhrAs nIleArgLys CysGlnG	luL euLeuGlu	Gl nLeuAsnGlv	200
J-3 2			

TGFb+MMP+ifn b Sequence

10	20	30	40	50	60	
1234567890 12345	67890 123456	7890 1234	567890 12345	67890 123456	7890	
AAGATCAACC TCACC	TACAG GGCGGA	CTTC AAGA	ICCCTA TOGAC	BATGAC GGAGAA	GATG 1020	
LysIleAsnL euThr	TyrAr gAlaAs	pPhe LysI	leProM etGlu	MetTh rGluLy	/sMet	
CAGAAGAGIT ACACT						
GlnLysSerT yrThr	AlaPh eAlaI	leGln GluM	etLeuG lnAsr	walph eLeuva	alPhe	
,						
AGAAACAATT TCTCC						
ArgAsnAsnP heSer	SerTh rGlyT	qaan GluT	hrIleV alVal	largle uleua:	spGlu	
			,	,		
CTOCACCAGC AGACA						
LeuHisGlnG lnThr	ValPh eLeuL	ysThr Vall	euGluG luLy:	sGlnGl uGluAı	gLeu	
3.00000003.03. momoo						
ACGIGGGAGA TGTOC						١.
ThrTrpGluM etSer	rSerTh rAlaL	euhis Leul	ysSerT yrTy:	rTrpAr gValG	lnArg	
TIN CYCHINA X X C HYYXHY	33.0m ozzor					
TACCITAAAC TCATO						١.
Tyrieulysl euMet	chysiy rasns	eriyr Ala'i	mmetv aiva	largal aGluI	LePhe	
אכיצא בתחוות מיצוני	Cammar andro		2000000 2222	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	0 1000	
AGGAACTITC TCATO					C 1376)
ArgAsnPheL euIle	errear dardr	eunr Arga	silnes inas	_		
				uga		

ifn+MMP+TGFb Sequence

10 20 30 40 50 60	
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890	
ATGAACAACA GGIOGATOCT OCACOCTOCG TETOCTOCTIGT OCTTCTOCAC CACAGOOCTC	60
Metasnasna rgTrpIleLe uHisalaala PheLeuLeuC ysPheSerTh rfhralaLeu	
TCCATCAACT ATAAGCAGCT CCAGCTCCAA GAAAGGACGA ACATTCGGAA ATGTCAGGAG	100
SerileAsnT yrlysGlnLe uGlnLeuGln GluArgThrA snIleArgLy sCysGlnGlu	120
Services in Army Service Continues on Continue Services of Service	
CTCCTGGAGC AGCTGAATGG AAAGATCAAC CTCACCTACA GGGGGGACTT CAAGATCCCT	180
LeuleuGluG lnLeuAsnGl ylysIleAsn LeufhrTyrA rgAlaAspPh elysIlePro	
ATGGAGATGA COGAGAAGAT GCAGAAGAGT TACACTGCCT TTGCCATCCA AGAGATGCTC	240
MetGluMetT hrGluLysMe tGlnLysSer TyrThrAlaP heAlaIleGl nGluMetLeu	
CAGANTGICI TICTIGICIT CAGAAACAAT TICTCCAGCA CIGGGIGGAA TGAGACIATT	300
GlnAsnValP heLeuValPh eArgAsnAsn PheSerSerT hrGlyTrpAs nGluThrIle	
GITGIAGGIC TOCKGGATGA ACKGCAGGAG CAGACAGIGI TICKGAAGAC AGIACTAGAG	360
ValValArgi, euleuAspGl uleuHisGln GlnThrValP heleuLysTh rValleuGlu	200
varvaningii Cancarapor ancuirosii Orininvari ilancuironi i variatata	
GAAAAGCAAG ACGAAACATT GACGTCCCGAG ATGTCCTCAA CTGCTCTCCA CTTGAAGAC	420
GlulysGlnG luGluArgle uThrTrpGlu MetSerSerT hrAlaLeuHi sLeuLysSer	
TATTACTOGA GOGTOCAAAG GTACCTTAAA CTCATGAAGT ACAACAGCTA COCCTOGATG	480
TyrTyrTrpA rgValGlnAr gTyrLeuLys LeuMetLysT yrAsnSerTy rAlaTrpMet	
GIGGICCGAG CAGAGAICTT CAGGAACTTT CTCATCATTC GAAGACTTAC CAGAAACTTC	540
ValValArgA laGluIlePh eArgAsnPhe LeuIleIleA rgArgLeuTh rArgAsnPhe	340
The second secon	
CAAAACGAAT TOGGGGGGG CGGATCOCCG CTCGGGCTTT GGGCGGGAGG GGGCTCAGCG	600
GlnAsnGluP heGlyGlyGl yGlySerPro LeuGlyLeuT rpAlaGlyGl yGlySerAla	
GCCCCACTAT CCACCIGCAA GACIATCGAC ATGGAGCIGG TGAAGCGGAA GCGCATCGAG	660
AlaAlaLeuS erThrCysLy sThrIleAsp MetGluLeuV allysArgLy sArgIleGlu	
	720
GCCATCOGOG GCCAGATOCT GTCCAAGCTG COGCTCGCCA GCCCCCCAG CCAGGGGGAG AlaIleArgG lyGlnIleLe uSerLysLeu ArgLeuAlaS erProProSe rGlnGlyGlu	120
rection of the total force of the state of t	
GIGCCCCCC GCCCCCIGCC CGAGGCCGIG CICGCCCTGT ACAACAGCAC CCCCCACCGG	780
ValProProG lyProLeuPr oGluAlaVal LeuAlaLeuT yrAsnSerTh rArgAspArg	
GIGGCCGGG AGAGIGCAGA ACCOGACCCC GAGCCIGAGG COGACIACIA CGCCAAGGAG	840
ValAlaGlyG luSerAlaGl uProGluPro GluProGluA laAspTyrTy rAlaLysGlu	
GICACCOGOG TOCTAATOGT GGAAACCCAC AACGAAATCT ATGACAAGTT CAAGCAGAGT	900
ValThrArgV alleuMetVa lGluThrHis AsnGluIleT yrAsplysPh elysGlnSer	200
variminies ameurecva totuliums asiatumen ynasphysm enysamsen	
ACACACAGCA TATATATGIT CITICAACACA TCAGAGCTCC GAGAAGCCGT ACCTGAACCC	960
ThrHisSerI leTynMetPh ePheAsnThr SerGluLeuA rgGluAlaVa lProGluPro	
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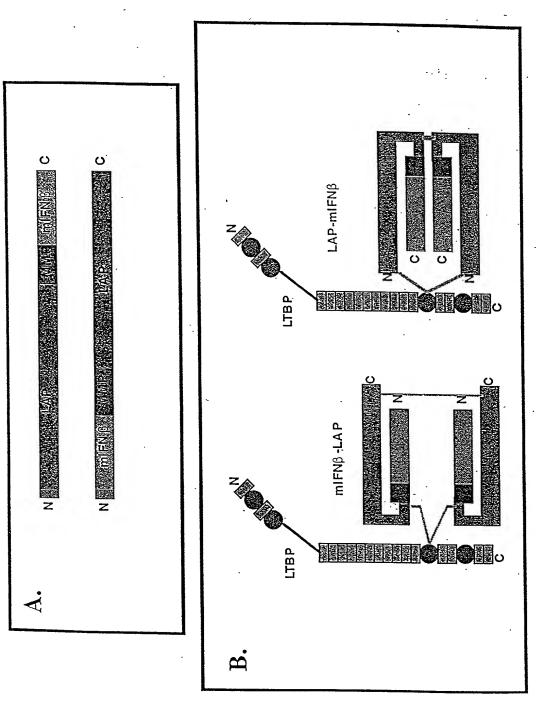
ifn+MMP+TGFb Sequence

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GIGITOCICT	CCCCGGGCAGA	GCTGCGTCTG	CTGAGGAGGC	TCAAGTTAAA	AGTGGAGCAG	1020
ValleuleuS	erArgAlaGl	uleuArgleu	LeuArgArgL	eulysLeuly	sValGluGln	
CACGTGGAGC	TGTACCAGAA	ATACAGCAAC	AATTCCTGGC	GATACCTCAG	CAACCGGCTG	1080
HisValGluL	euTyrGlnLy	sTyrSerAsn	AsnSerTrpA	rgTyrLeuSe	rAsnArgLeu	
CIGGCACCCA	COCACTOCC	AGAGTÖGTTA	TCTTTTGATG	TCACCGGAGT	TGTGCGGCAG	1140
LeuAlaProS	erAspSerPr	oGluTrpLeu	SerPheAspV	alThrGlyVa	lValArgGln	
TOGTTGAGOC	GTGGAGGGGA	AATTGAGGGC	TTTOGOCTTA	GOGGCCACTG	CTCCTGTGAC	1200
TrpLeuSerA	rgGlyGlyGl	ulleGluGly	PheArgLeuS	erAlaHisCy	sSerCysAsp	
AGCAGGGATA	ACACACIGCA	AGTGGACATC	AACCGGTTCA	. CTACCGCCCG	COGAGGIGAC	1260
SerArgAspA	smihrleuGl	nValAspIle	AsnGlyPheT	hrThrGlyAr	gArgGlyAsp	
CIGGCCACCA	TTCATGGCAT	GAACCGGCCT	TICCICTIC	TCATGGCCAC	CCCCCTCCAG	1320
LeuAlaThrI	leHisGlyMe	tAsnArgPro	Pheleuleul	euMetAlaTh	rProLeuGlu	
AGGGCCCAGC	ATCTGCAAAC	Ctga/ICI/AGA	ω			1352
	I isLeuGlnSe					

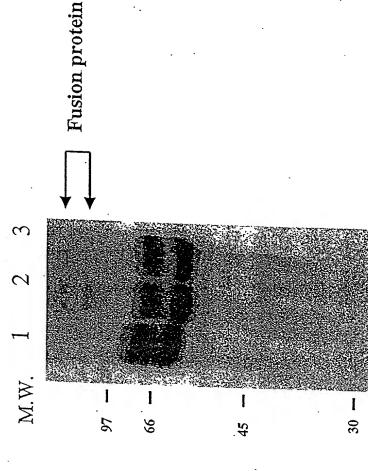
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Hu TGF-# T
              MPPSGLRLLPLLLPLLWLLV-LTPGPPAAGLSTCKT1DMELYKRKR1EA1RGOILSKLRLASPPSGGE-VP-PGP
 HU TGF-B 2
              MHYCYLSAFLILH LYTVAL-----SUSTCSTLDMOQFMRKRIEAIRGQILSKLKLTSPP---EDYPEPEE
 Hu IGF-8 3
              MKHHLORALVVLALLNFATVSL-----SLSTCTTLDFGHIKKKRVEAIRGOILSKLRLTSPP---EPTV-MIH
 CK TGF-B 4
 Fg IGF-8 5
              MEY------LIMLLVLLV-LHESSLAMSLSTCKAVDHEEVRKRRIEAIRGOILSKLKLDKTPDVDS-EK-MTY
                                                 100
Hu TGF-# 1
              LPEAVLALYMSIRORVAGESAEPE-PEP------EADYYAKEVIRVLHV----ETHNEIYDKFKOSTHSIYMFF
 HU TGF-# Z
              VPPEVISIYHSTROLL - OEKASR-RAAACERERSDEEYYAKEVYKIDMPPFFPS-EHAIPPTFYRPY-FRIVRF
 Hu TGF-# 3
              VPYOVLALYMSTRELL--EEHGER-KEEGCTOEHTESEYYAKEIHKFDMIOGLAE-HHELAYCPKGIT-SKVFRF
 Ck TGF-B 4
              -----GSPU-RPP-GIAPUSIG-SR--RA
· fg TGF-# 5
              PSEAIF-LYMSTLE-VIREKATRE-EEEHVGHDOHJODYYAKOYYRF----ESITELEDHEFKFK--------
                  140
              NTSEL-----RE-AVPEPVLLS-RAELRLERLEL----KV-EOHVELYG-----KYSNHSURYLSHRLLAPSDSPE
 Hu TGF-8 1
              DVSA-----HEK<u>HAS</u>NLV-KAEFRVFRLORPK-ARVPEORIELYOILKSKDLISPTORYIDSKVVKTRAEGE
 HU TGF-8 2
 Ku TGF-# 3
              <u>KYSS-------VEKNRT</u>NLF-RAEFRYLRYP<u>NPS</u>-SKRNEORIELFOILRP-DEHIAKORYIGGKHLPTRGTAE
Ck TGF-B 4
              TASSSCSTSSRYRAEVGGRALLHRAELRHLROKAAADSAGTEORLELYOGYG-----<u>HAS</u>URYLHGRSVRATAODE
 Fg TGF-B 5
              <u>#ASHV-----RENYGHN-SLLH-HAELRHYK-KOTO--KNNOORHELFU--KYOEHGT</u>THSRYLESKYTTPVTODE
                                       220
              WLSFDVFGVVROWLSRGGE1EGFRLSAHCSG -------DSRDHTLOVDIN-GFTTGR-------RGDLAT1-----
 Hu TGF-B 1
              WLSFDYTDAVHEWLHHKDRNLGFKISLHCPCCTFVPSNNYLIPHKSEELEARFA-GIDGISTYTSGOOKTIKSTRK
 HU TGF-$ 2
 HU TGF-# 3
              WLSFDYTDTYREVLLRRESHLGLEISIHCPCHTFOP-NGDILEHIHEYMEIKFK-GVONEDDHGRGDLGRLK---K
 Ck TGF-# 4
              WLSFDYTDAVHOULSGSELLGYFKLSVHCPCEMGPG-HADEHRISIEGFEOQ------RGDHOSIA---K
 fg TGF-# 5
              INSTDVTKTVNEHLKRAEENEOFGLOPACKC#------PTPQAKD----ID1EGFPAL-RGOLASL--SSK
                           260
                                                                          -300
                                                   1 580
 HU TGF-# 1
              ----HGMNRPFLLLMATPLERA-OH--LOSS---RHRRALDTNYCFSST--EKNCCVROLYIDFRKDLGWKWIHEP
 Hu TGF-B 2
              KHSGKT---PHLLIHLLPSYRL-ESQ----OTHRRKKRALDAAYCFRNY--ODHCCLRPLYIDFKRDLGUKWIHEP
 Hu TGF-B 3
              QKONN--N-PKLILMMIPPHRI-DNPGOGGQ---RKKRALDINYCFRNL--EENCCVRPLYIDFRODLGWKWYHEP
 Ck TGF-8 4
              *KHRR**V-PYVLAMALPAERANE***LHSA****RRRQLDTDYCFGPGTDEKNCCVRPLY1DFRKDLQHKW1HEP
 Fg TGF-8 5
              ENT -----KPYL --MITSHPAERIDTYT SS --- RKKRGYGQEYCFGNN -- GPHCCVKPLYINFRKOLGNKV1HEP
                   320
                                       340
                                                           360
                                                                               380
                                                                                         390
 Ru TGF-# 1
              KGYHANFCLGPCPYTWSLDTOYSKVLALYNOHNPGASAAPCCVPQALEPLPTVYYVGRKPKVEQLSNHTVRSCKCS
 Hu TGF-# 2
              KGYNANFCAGACPYLYSSDTOHSRYLSLYNTENPEASASPCCVSODLEPLTILYYLGKIPKIEOLSNHLVKSCKCS
 Ku TGF-$ 3
              KGYYAHFCSGPCPYLRSADTTHSTYLGLYHTLHPEASASPCCYPODLEPLTILYYYGRIPKYEOLSHMYYKSCKCS
 Ck TGF-B 4
              KGYHANFCHGPCPYTUSADTOYTKVLALYHOHNPGASAAPCCVPGTLDPLPTTYVGRNYRVEOLSHHVVRACKCS
 fg TGF-β 5
              KGYEANYCLGNCPYIWSHOTOYSKYLSLYHOHNPGASISPCCVPOVLEPLPIIYYVGRIAKVEOLSHMYVRSCHCS
```

Protein _	rin Sequence	
MMP-I/MMP-8		
Human type I collagen (α1)	Ala-Pro-Gln-Gly775~Ile776-Ala-Gly-Gln	80
Human type I collagen (α2)	Gly-Pro-Gln-Gly775~Leu776-Leu-Gly-Ala	80
Human type II collagen	Gly-Pro-Gin-Gly775~Leu776-Ala-Gly-Gln	80
Human type III collagen	Gly-Pro-Leu-Gly715~Ile716-Ala-Gly-Ile	80
Hūman α ₂ -macroglobulin	Gly-Pro-Glu-Gly679~Leu680-Arg-Val-Gly	84
Rat a2-macroglobulin	Ala-Ala-Tyr-Hises ~ Leuesz Val-Ser-Gln	84
Rat az-macroglobulin	Met-Asp-Ala-Phe691~Leu692-Glu-Ser-Ser	84
Rat \alpha_1-macroglobulin	Glu-Pro-Gln-Ala ₆₈₃ ~Leu ₆₈₄ -Ala-Met-Ser	84
Rat at-macroglobulin	Gln-Ala-Leu-Ala685~Met686-Ser-Ala-Ile	84
Chicken ovostatin	Pro-Ser-Tyr-Phe673~Leu674-Asn-Ala-Gly	79
Human pregnancy zone protein	Tyr-Glu-Ala-Glyss5~Leusss-Gly-Val-Val	84
	Ala-Gly-Leu-Gly657~Valose Val-Glu-Arg	84
Human pregnancy zone protein	Ala-Gly-Leu-Gly-757~ lle-758-Ser-Ser-Thr	84
Human pregnancy zone protein	Gly-Ala-Met-Phe ₃₅₂ ~Leu ₃₅₃ -Glu-Ala-Ile	85
α ₁ -Protease inhibitor	lle-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	86
Human aggrecan	Thr-Glu-Glu-Glu ₂₇₃ ~Ala ₂₇₄ -Arg-Gly-Ser	86
Human aggrecan		87
Human cartilage link	Arg-Ala-Ile-His ₁₆ ~ Ile ₁₇ -Gln-Ala-Glu	- 88
Human insulin-like growth factor	Leu-Arg-Ala-Tyroo-Leu100-Leu-Pro-Ala	- 68
binding protein-3		
MMP-2 Guinea pig α1(I) gelatin	Gly-Ala-Hyp-Gly ₅₄₇ ~Leu ₅₄₈ -Glx-Gly-His	24
Rat \all(l) gelatin	Gly-Pro-Gln-Gly ₁₉₀ ~Val ₁₉₁ -Arg-Gly-Glu	30
•	Gly-Pro-Ala-Gly ₂₇₇ ~Val ₂₇₈ -Gln-Gly-Pro	30
Rat α1(1) gelatin Rat α1(1) gelatin	Gly-Pro-Ser-Gly ₃₀₁ ~Leu ₃₀₂ -Hyp-Gly-Pro	30
	Gly-Pro-Ala-Gly331~Glu332-Arg-Gly-Ser	30
Rat α1(I) gelatin Rat α1(I) gelatin	Gly-Ala-Lys-Gly ₃₆₁ ~Leu ₃₆₂ -Thr-Gly-Ser	30
-	Gly-Pro-Ala-Gly ₃₈₂ ~Gln ₃₈₃ -Asp-Gly-Pro	30
Rat α1(I) gelatin	Gly-Pro-Ala-Gly ₆₃₄ ~Phe ₆₃₅ -Ala-Gly-Pro	30
Rat α1(I) gelatin Rat α1(I) gelatin	Gly-Pro-Ile-Gly ₆₇₆ ~Asn ₆₇₇ -Val-Gly-Ala	30
	Gly-Pro-Hyl-Gly685~Ser686-Arg-Gly-Ala	30
Rat \all(1) gelatin	Gly-Pro-Gln-Gly ₇₇₅ ~lle ₇₇₆ -Ala-Gly-Gln	22
Bovine type I collagen (a1)	Gly-Pro-Gln-Gly775~Leu776-Leu-Gly-Ala	22
Bovine type I collagen (a2)	Ile-Pro-Glu-Asn ₃₄₁ ~Phe ₃₄₂ -Phe-Gly-Val	89
Human aggrecan	Pro-Pro-Gly-Ala ₆₂ ~Tyr ₆₁ -His-Gly-Ala	90
Human galectin-3	· · · · · · · · · · · · · · · · · · ·	. 87
Human cartilage link	· Arg-Ala-IIe-His ₁₆ ~IIe ₁₇ -GIn-Ala-Glu Gly-Pro-His-Leu ₂₅ ~Leu ₂₆ -Val-Glu-Ala	87
Human cartilage link Human insulin-like growth factor	Leu-Arg-Ala-Tyrs9~Leu ₁₀₀ -Leu-Pro-Ala	88
binding protein-3	Ecu-Aig-Aia-1 Jigg - Eculon-Ecu-110-Aia	00
MMP-3	ć	•
Human α ₂ -macroglobulin	Gly-Pro-Glu-Gly679~Leu680-Arg-Val-Gly	79
Human α ₂ -macroglobulin	Arg-Val-Gly-Phe684~Tyr685-Glu-Ser-Asp	79
Human α_1 -macrogrounn Human α_1 -antichymotrypsin	Leu-Leu-Ser-Ala360~ Leu361-Val-Glu-Thr	91
α ₁ -protease inhibitor	Glu-Ala-Ile-Pro357~Met358-Ser-Ile-Pro	91
Antithrombin III	lle-Ala-Gly-Argass~Ser38-Leu-Asn-Pro	91
	Leu-Asn-Ala-Gly ₆₇₇ ~Phe ₆₇₈ -Thr-Ala-Scr	79, 92
Chicken ovostatin	Ile-Pro-Glu-Asn ₃₆₁ ~Phe ₃₄₂ -Phe-Gly-Val	93
Human aggrecan Substance P	Lys-Pro-Glu-Gin ₆ ~Phe ₇ -Phe-Gly-Leu	37
Human ProMMP-1	Asp-Val-Ala-Gln ₈₀ ~Phe ₈₁ -Val-Leu-Thr	43
		94
Human ProMMP-3	Asp-Thr-Leu-Gluss ~ Valso-Met-Arg-Lys	- 94
Human ProMMP-3	Asp-Val-Gly-His ₁₂ ~Phe ₈₃ -Arg-Thr-Phe	95
Human ProMMP-8	Asp-Ser-Gly-Gly ₁₈ ~Phe ₇₉ -Met-Leu-Thr	48
Human ProMMP-9	Arg-Val-Ala-Glu ₄₀ ~Met ₄₁ -Arg-Gly-Glu	48
Human ProMMP-9	Asp-Leu-Gly-Arg ₈₇ ~Phe ₈₈ -Gln-Thr-Phe	~1 ∪

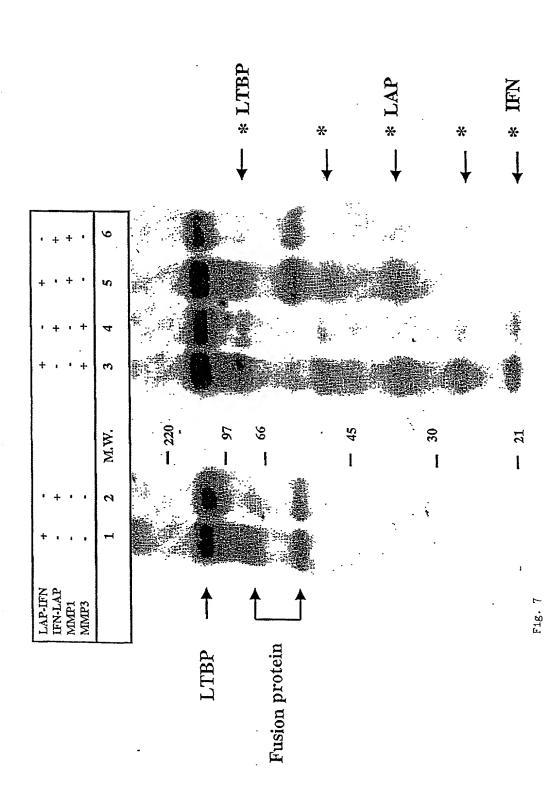
_	Sequence	Reference
human insulin-like growth factor	Leu-Arg-Ala-Tyt ₉₉ ~ Leu ₁₀₀ -Leu-Pro-Ala	88
binding protein-3	Ala-Pro-Gly-Asnion ~ Alairo-Ser-Glu-Ser	88
· · · · · · · · · · · · · · · · · · ·	Phe-Ser-Ser-Glu176~Ser177-Lys-Arg-Glu	88
Bovine a1(II) collagen. N-telopoptide	Ala-Gly-Gly-Ala115~Gln116-Met-Gly-Val	96
dovine αI(II) collagen. N-telopeptide	Gln-Mct-Gly-Val110~Mct120-Gln-Gly-Pro	96
Bovine a1(IX) collagen, NC2	Met-Ala-Ala-Ser~Leu-Lys-Arg-Pro	96
Bovine α2(1X) collagen, NC2	~Ala-Lys-Arg-Glu	96
Bovine a3(IX) collagen, NC2	~Leu-Arg-Lys-Pro	96
Bovine α I(XI) collagen, N- telopeptide	Gin-Ala-Gin-Ala~ile-Leu-Gin-Gin	96
Human cartilage link	Arg-Ala-Ile-Histo~llet-Gln-Ala-Glu	87
Bovine insulin, B chain	Leu-Val-Glu-Alan-Leu15-Tyr-Leu-Val	97
Bovine insulin, B chain	Glu-Ala-Leu-Tyris~Leuir-Val-Cys-Gly	21,97
MMP-7	***	•
Human aggrecan	lle-Pro-Glu-Asnus-Pheur-Phe-Gly-Val	89
Human cartilage link	Gly-Pro-His-Leu25~Leu26-Val-Glu-Ala	87
Human prourokinase	Pro-Pro-Glu-Glu143~Leu144-Lys-Phe-Gln.	98
MMP-9	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
Human type V collagen (α1)	Gly-Pro-Pro-Gly439~Val440-Val-Gly-Pro	99
Human type V collagen (α2)	Gly-Pro-Pro-Gly415~Leu446-Arg-Gly-Glu	99
Human type XI collagen (α1)	Gly-Pro-Gly-Gly439~Val440-Val-Gly-Pro	9 9
Human aggreçan	Ile-Pro-Glu-Asn341~Phe342-Phe-Gly-Val	89
Human galectin-3	Pro-Pro-Gly-Ala62~Tyr63-His-Gly-Ala	. 90
Human cartilage link	Arg-Ala-Ile-His16~Ile17-Gln-Ala-Glu	87
MMP-10		
Human cartilage link	Arg-Ala-Ile-His16~Ile17-Gln-Ala-Glu	87
Human cartilage link	Gly-Pro-His-Leu25~Leu26-Val-Glu-Ala	87

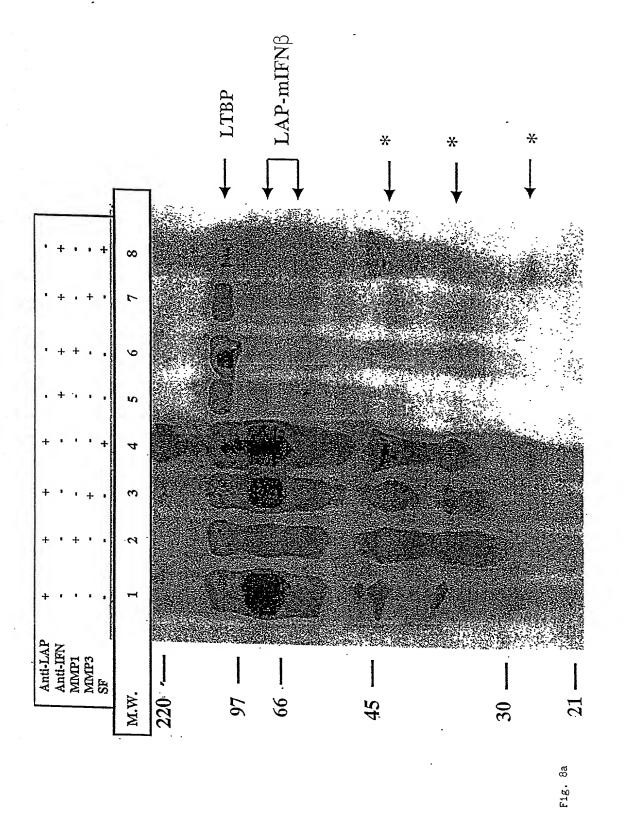


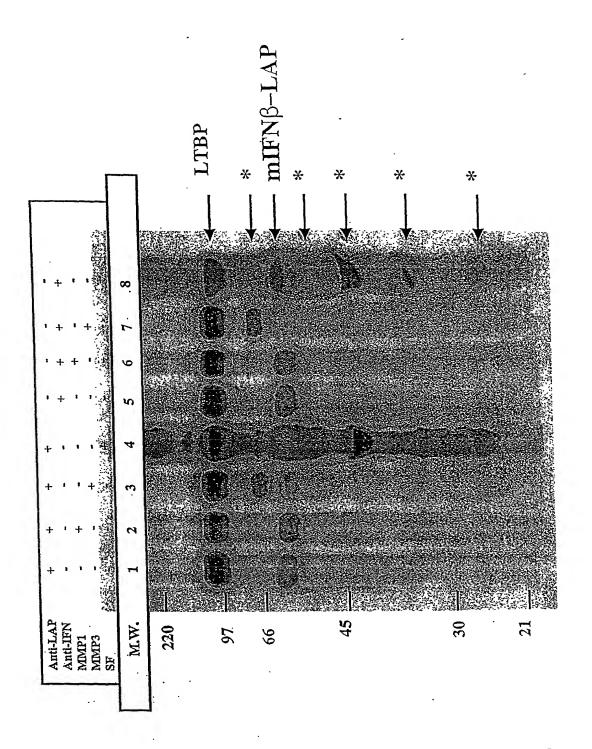
F18. 5



F18.

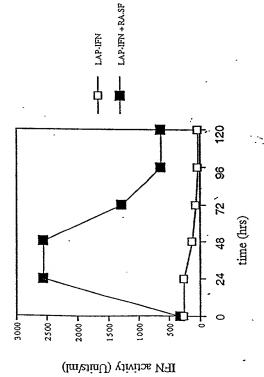




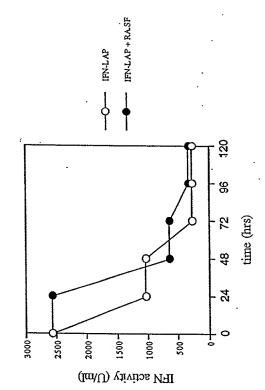


F1g. 8b

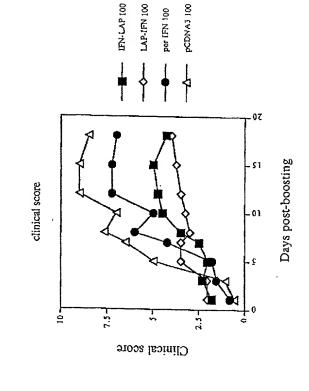




M M



18.9



paw swelling

The porter 100

The porter 100

32.5-

(I-01xmm) gnillaws waq

22,5-

27.5

Days post boosting